Introduction

*Cepaea nemoralis* is a common European land snail which has been the subject of many studies. These species can be treated as convenient model organisms because of their little dispersion , therefore genetic patterns are localised within a particular area.

Shell colours and banding patterns of *C. nemoralis* are highly variable (Kerney and Cameron 1979). Snails can have pink, yellow or brown background with a number of bands varying from zero to five. The difference in colours can give them camouflage abilities to avoid the predation. This characteristic can be a reason of different observed phenotypic frequencies in various habitats. Previous studies about the relationship between morph and habitat states that that shell colour shows stronger and more consistent variation within habitats than banding patterns do. Yellow-coloured snails are found more often in open habitats such as grasslands and at lower altitudes. However, brown-coloured snails are more distributed in Woodlands and hidden locations where they can conceal their presence against enemies. We also consider the dark brown peristome lip around the aperture of the shell as an evidence of adult snail maturity, but not as the evidence of polymorphism.

During the sampling 6 different snail habitats will be considered (e.g. beech woods, oak woods , mixed deciduous woods, hedgerows, rough herbage, short turf).A Chi square test can be used to analyse the data collected in order to determine the significant difference between the phenotypic frequencies at different locations.

The aim of our group study is to determine whether evolutionary processes have an impact on distribution *of C.nemoralis*. Despite the intensity of polymorphism studies, the main factor affecting the variability between C.nemoralis is still the matter of controversy. The main rationalisations for these processes were genetic drift, natural selection, random mutation and spread or loss of these specific alleles responsible for observed features within the population. According to different selection pressures, certain phenotypes can be observed only at specific locations. The variation within the phenotypic frequency could be also due to gene flow, a migration of genes from one population to the other within the same species.

According to the previous studies, a specific conclusion can’t be made about which of the evolutionary processes have affected the allele frequency and location distribution of snails , as the factors affecting the population were not known before the sampling. For the improvement of the experiment accuracy such factors as temperature, human activity, predation, climate change could be taken into the account. However, the study of *C.nemoralis* can help to determine